

**Appl. No.** : **09/581,651**  
**Filed** : **October 10, 2000**

#### **AMENDMENTS TO THE DRAWINGS**

Figure 2 has been amended to correct the reference to pMSF-1 $\alpha$ . Figure 3 has been amended in accordance with the Replacement Sequence Listing. Clean copies of Figures 2 and 3 and redlined copies of Figures 2 and 3 are enclosed. Formal drawings will be submitted upon approval of the amendments of Figures 2 and 3.



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	10	20	30	40	50	60
pMSF-1 $\alpha$	NLVATCLPVRASLP	HLRLNMLRGPGPGLLL	LAVQCLGTAVPSTG	ASKSKRQAQQMVQP	QSP	
fibronectin	NLVATCLPVRASLP	HLRLNMLRGPGPGLLL	LAVQCLGTAVPSTG	ASKSKRQAQQMVQP	QSP	
		10	20	30	40	
	70	80	90	100	110	120
pMSF-1 $\alpha$	VAVSQSKPGCYDNG	KHYQINQWERTYLG	NALVCTCYGSGRG	FNCSKPEABETCF	DKYT	
fibronectin	VAVSQSKPGCYDNG	KHYQINQWERTYLG	NVNLVCTCYGSGR	FNCSKPEABETCF	DKYT	
	50	60	70	80	90	100
	130	140	150	160	170	180
pMSF-1 $\alpha$	GNTYRVGDTYERPK	DSMIWDCTCIGAGR	GRISCTIANRCHEG	GQSYKIGDTWRRP	HETGG	
fibronectin	GNTYRVGDTYERPK	DSMIWDCTCIGAGR	GRISCTIANRCHEG	GQSYKIGDTWRRP	HETGG	
	110	120	130	140	150	160
	190	200	210	220	230	240
pMSF-1 $\alpha$	YMLECVCLGNGKG	EWTKPIAEKCFDHA	AGTSYVVGETWEK	PHYQGWMMVDCTC	LGEGSGR	
fibronectin	YMLECVCLGNGKG	EWTKPIAEKCFDHA	AGTSYVVGETWEK	PHYQGWMMVDCTC	LGEGSGR	
	170	180	190	200	210	220
	250	260	270	280	290	300
pMSF-1 $\alpha$	ITCTSRNRCNDQD	TRTSYRIGDTWSK	KNRGNLLQCICTG	NGRGEWK CERHTS	VQTTSSG	
fibronectin	ITCTSRNRCNDQD	TRTSYRIGDTWSK	KNRGNLLQCICTG	NGRGEWK CERHTS	VQTTSSG	
	230	240	250	260	270	280
	310	320	330	340	350	360
pMSF-1 $\alpha$	SGPFTDVRAAVYQ	PQPHQPPPYGHC	VTDSGVVYSVGMQ	WLKTQGNKQMLCT	CLGNGVSC	
fibronectin	SGPFTDVRAAVYQ	PQPHQPPPYGHC	VTDSGVVYSVGMQ	WLKTQGNKQMLCT	CLGNGVSC	
	290	300	310	320	330	340
	370	380		390	400	
pMSF-1 $\alpha$	QETAVTQTYGGNS	NGEPCVLPFTYNDRT	-----	DSTTSNYEQDQKYS	FCT	
fibronectin	QETAVTQTYGGNS	NGEPCVLPFTYNGRT	FYSCTTEGRQDGH	LWCSTTSNYEQDQKYS	FCT	
	350	360	370	380	390	400
	410	420	430	440	450	460
pMSF-1 $\alpha$	DHTVLVQTRGGNS	NGALCHFPFLYNN	HNHYTDCTSEGR	RDNMKWCGTTQNY	DADQKFGFCP	
fibronectin	DHTVLVQTRGGNS	NGALCHFPFLYNN	HNHYTDCTSEGR	RDNMKWCGTTQNY	DADQKFGFCP	
	410	420	430	440	450	460

*Fig. 2 (part 1)*

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	470	480	490	500	510	520
pMSF-1 $\alpha$	MAAHEEICTTNEGVMYRIGDQWDKQHDMMRCTCVGNRGGEWTCIAYSQLRDQCIVDD					
fibronectin	MAAHEEICTTNEGVMYRIGDQWDKQHDMMRCTCVGNRGGEWTCYAYSQLRDQCIVDD					
	470	480	490	500	510	520
	530	540	550	560	570	580
pMSF-1 $\alpha$	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTTFYQIGDSWEKYVHG					
fibronectin	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTTFYQIGDSWEKYVHG					
	530	540	550	560	570	580
	590	600	610	620	630	640
pMSF-1 $\alpha$	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPOPSHISKYI					
fibronectin	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPOPSHISKYI					
	590	600	610	620	630	640
	650	660	670	680	690	700
pMSF-1 $\alpha$	LRWRPVSIPPRNLGYXVSXSXYQFXWFLFFPAFEPTTLINYSYSIYYICLVNKQYVVNXID					
	:   →					
	(SEQ IS NO.: 37)					
fibronectin	LRWRPKNSVGRWKEATIPGHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTST					
	650	660	670	680	690	700
	(SEQ IS NO.: 44)					

*Fig. 2 (part 2)*

SEQ ID NO:	Sequence Type	Binding Site
[SEQ ID NO: 13]	5' untranslated region	
[SEQ ID NO: 14]	Signal	
[SEQ ID NO: 15]	NH2-terminal segment	
[SEQ ID NO: 16]	I	
[SEQ ID NO: 38]	I	Fibrin
[SEQ ID NO: 39]	I	Heparin
[SEQ ID NO: 40]	I	S. aureus
[SEQ ID NO: 17]	I	
[SEQ ID NO: 18]	Connecting strand	
[SEQ ID NO: 19]	I	
[SEQ ID NO: 20]	II	
[SEQ ID NO: 28]	II	Gelatin
[SEQ ID NO: 21]	I	
[SEQ ID NO: 22]	I	
[SEQ ID NO: 23]	I	
[SEQ ID NO: 24]	III	
[SEQ ID NO: 25]	Unique Sequence	
[SEQ ID NO: 29-33]	3' untranslated region	

NLVATCLPVRASLPHRLN  
 1MLRGPGGLLLAVQCLGTAVPSTGASKSKR  
 32QAQMVQPQSPVAVSQSKPG  
 52CYDNGKHYQINQWERTYVLGNALVCTCYGSGRGNCESKPEAEET  
 97GFDKYTGTNRVGDYERPKDSMIWDCTCIGAGRISCTIANR  
 141CHEGGSYKIGDTRRRPHETGGYMLECVCLGNGKGWTCCKPIAEK  
 186CFDHAAGTSYVVGETWEKPYQGMVMDCTCLGEGSGRITGTSRNR  
 232CNDQDTRTSYRIGDTWSKKDNRGNLLQCICITGNRGGEWKCEER  
 273HTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGH  
 305CVTDGSGVYVSGMQWLKTQGNKQMLCTCLGNGVSCQE  
 345TAVTQTYGNSNGEPCVLPFTYNDRTDSTTSNVEQDQKYSFCTDH  
 390FVLVQTRGNSNGALCHFPFLYNNHNYTDCITSEGRDRDNMKWCGTT  
 QNYDADQKFGFCPMAAHEEI  
 455CTTNEGVMYRIGDQWDKQHDGMHMRCTCVNGRGGEWTCIAYSQLRDQ  
 503CIVDDITYNVNDTFHKRHEEGHMLNCTCFQGRGRWKCDPVDQ  
 545CODSETGTFYQIGDSWEKYVHGVRVYQCYCYGRGIGEWHCQPLQTYPSS  
 594SGPVEVFITETPSQPNSHPIQWNAPOPSHISKYILRWRP  
 633VSIPPRNLGY  
 \*VS\*SYQF\*WFLFFPAFEPPTLLINYSIYYICLVNKQYVVN\*IDL\*TEKKKKK[SEQ ID NO: 29-33]3' untranslated region

Figure 3

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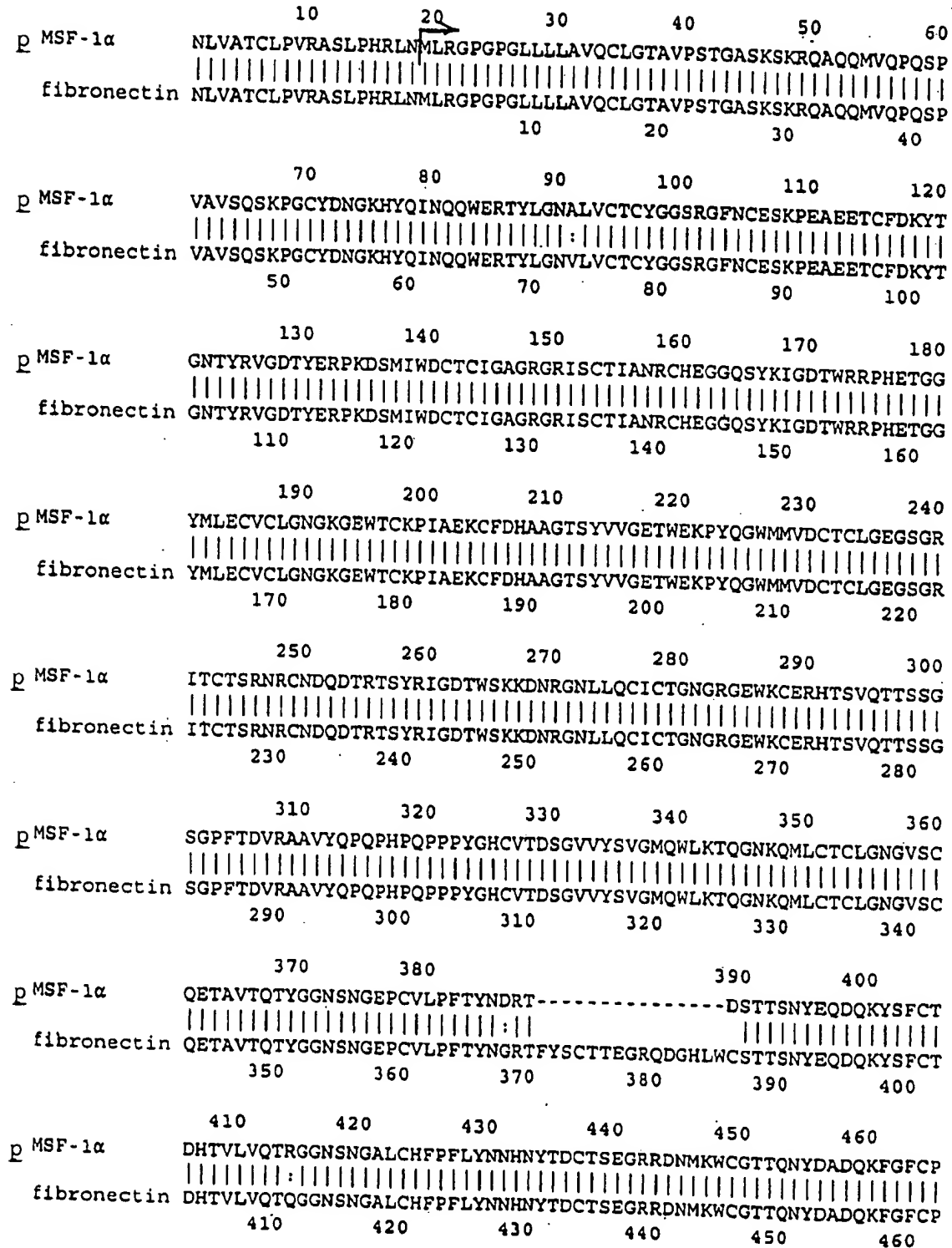


Fig. 2 (part 1)

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	470	480	490	500	510	520
pMSF-1 $\alpha$	MAAHEEICTTNEGVMYRIGDQWDKQHDMMRCTCVGNRGGEWTCIAYSQLRDQCIVDD					
fibronectin	MAAHEEICTTNEGVMYRIGDQWDKQHDMMRCTCVGNRGGEWTCYAYSQLRDQCIVDD					
	470	480	490	500	510	520
	530	540	550	560	570	580
pMSF-1 $\alpha$	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGWKCDPVDQCQDSETGTFTYQIGDSWEKYVHG					
fibronectin	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGWKCDPVDQCQDSETGTFTYQIGDSWEKYVHG					
	530	540	550	560	570	580
	590	600	610	620	630	640
pMSF-1 $\alpha$	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAQPQSHISKYI					
fibronectin	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAQPQSHISKYI					
	590	600	610	620	630	640
	650	660	670	680	690	700
pMSF-1 $\alpha$	LRWRPVSIPPRNLGYKVSXSXYQFXWFLFFPAFEPTTLINYSYSIYYICLVNKQYVVNXID					
	:   →					

(SEQ IS NO.: 37)

fibronectin	LRWRPKNSVGRWKEATIPGHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDETTTST
	650 660 670 680 690 700

(SEQ IS NO.: 44)

*Fig. 2 (part 2)*

SEQ ID NO:	Sequence Type	Binding Site
[SEQ ID NO: 13-19]	5' untranslated region	
[SEQ ID NO: 14-20]	Signal	
[SEQ ID NO: 15-21]	NH2-terminal segment	
[SEQ ID NO: 16-22]	I	
[SEQ ID NO: 18-23]	I	Fibrin
[SEQ ID NO: 19-24]	I	Heparin
[SEQ ID NO: 20-25]	I	S. aureus
[SEQ ID NO: 17-26]	I	
[SEQ ID NO: 18-27]	Connecting strand	
[SEQ ID NO: 19-28]	I	
[SEQ ID NO: 20-29]	II	
[SEQ ID NO: 28-30]	II	Gelatin
[SEQ ID NO: 21-31]	I	
[SEQ ID NO: 22-32]	I	
[SEQ ID NO: 23-33]	I	
[SEQ ID NO: 24-34]	III	
[SEQ ID NO: 25-35]	Unique Sequence	
[SEQ ID NO: 29-33 36-40]	3' untranslated region	

NLVATCLPVRASLPHRLN

1<sup>ML</sup>RGPGPGLLLLAVQCLGTAVPSTGASKSKR

32<sup>QAQ</sup>QMVQPOQSPVAVSQSKPG

52<sup>CYD</sup>NGKHYQINQOWERTYLGNAIVCTCYGSGRGFNCESKPEAEET  
 97<sup>CFD</sup>KYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRI SCTIANR  
 141<sup>CHE</sup>GGQSYKIGDWRPHETGGYMLECVCLNGKGGEWTKFPAEK  
 186<sup>CFD</sup>HAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITGTSRNR  
 232<sup>CND</sup>QDTRTSYRIGDTWSKKDNRGNLLQICICTGNRGGEWKGER

273<sup>HTS</sup>VQTTSSGSGPFTDVRAAVYQPPHPQPPYGH

305<sup>CVT</sup>DSGVVYSVGMQWLKTQGNKQMLCTCLNGVSCQE

345<sup>TAV</sup>TQTYGGSNGEPCVLPFTYNDRTDSTTSNYEQDQKYSFCTDH  
 390<sup>TVL</sup>VQTRGGSNGALCHFPFLYNNHNYTDCTSEGRDRNMKWCGETT  
 QNYDADQKFGFCPMAHEEI

455<sup>CTT</sup>NEGVMYRIGDQWDKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQ  
 503<sup>CIV</sup>DDITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQ  
 545<sup>CQD</sup>SETGTIFYIGDSWEKYVHGVRYQCYCYGRGIGEHWCQPLQTYPSS

594<sup>SGP</sup>VEVFITETPSQPNSHPIQWNAQPSHISKYILRWRP

633<sup>VS</sup>IPPNLGY

\*VS\*SYQF\*WELFFPAFEPTLINYSYIYICLVNKQYVNN\*IDL\*TEKKKKK [SEQ ID NO: 29-33 36-40] 3' untranslated region

Figure 3